



SEQUENCE LISTING

<110> H. Robert  
Hengartner, Michael

<120> IDENTIFICATION AND CHARACTERIZATION OF A  
GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND  
USES THEREOF

<130> 01997/201006

<140> US 09/993,420

<141> 2001-11-06

<150> 09/234,186

<151> 1999-01-20

<150> 07/898,933

<151> 1992-06-12

<150> 07/927,681

<151> 1992-08-10

<150> 08/288,295

<151> 1994-08-10

<150> 08/801,248

<151> 1997-02-19

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Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln				
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gac ttg cca tca ccg agt agg cag gct tcg acg cga aga atg tcc atc				192
Asp Leu Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile				
	50	55	60	
gga gag tca att gat gga aaa atc aat gat tgg gaa gag cca agg ctt				240
Gly Glu Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu				
	65	70	75	
gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa				288
Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln				
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aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa				336
Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln				
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ccg gag cac gaa atg atg cga gtt atg gga acg ata ttc gag aag aag				384
Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys				
	115	120	125	
cac gcg gaa aat ttt gag acc ttc tgt gag cag ctg ctc gca gtg ccc				432
His Ala Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro				
	130	135	140	
aga atc tca ttt tca ctg tat cag gat gtg gtt cgg acg gtt gga aat				480
Arg Ile Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn				
	145	150	155	
gca cag aca gat caa tgt cca atg tct tat gga cgt ttg ata ggt cta				528
Ala Gln Thr Asp Gln Cys Pro Met Ser Tyr Gly Arg Leu Ile Gly Leu				
	160	165	170	
atc tcg ttc ggc ggt ttc gta gct gca aaa atg atg gaa tcc gtg gaa				576
Ile Ser Phe Gly Gly Phe Val Ala Ala Lys Met Met Glu Ser Val Glu				
	175	180	185	190
ctg cag gga caa gtg cga aac ctc ttc gtt tac aca tcg ctg ttc atc				624
Leu Gln Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile				
	195	200	205	
aaa acg cgg atc cgc aac aac tgg aag gaa cac aat cgg agc tgg gac				672
Lys Thr Arg Ile Arg Asn Asn Trp Lys Glu His Asn Arg Ser Trp Asp				
	210	215	220	
gac ttc atg aca ctc gga aaa caa atg aaa gag gac tac gaa cga gca				720
Asp Phe Met Thr Leu Gly Lys Gln Met Lys Glu Asp Tyr Glu Arg Ala				
	225	230	235	
gaa gct gaa aaa gtg gga cgc cgg aag cag aac aga cgg tgg tcg atg				768
Glu Ala Glu Lys Val Gly Arg Arg Lys Gln Asn Arg Arg Trp Ser Met				
	240	245	250	

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 Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile Gly Glu  
 50 55 60  
 Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu Asp Ile  
 65 70 75 80  
 Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln Asn Gly  
 85 90 95  
 Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln Pro Glu  
 100 105 110  
 His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys His Ala  
 115 120 125  
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 Ser Phe Ser Leu Tyr Gln Asp Val Val Arg Thr Val Gly Asn Ala Gln  
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 225 230 235 240  
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 Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln  
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gac ttg cca tca ccg agt agg cag gct tcg acg cga aga atg tcc atc 192  
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gga gag tca att gat gga aaa atc aat gat tgg gaa gag cca agg ctt 240  
 Gly Glu Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu  
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gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa 288  
 Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln  
                           80                          85                          90

aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa 336  
 Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln  
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 Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys  
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 Leu Gln Gly Gln Val Arg Asn Leu Phe Val Tyr Thr Ser Leu Phe Ile  
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 Tyr Arg Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly  
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 Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln  
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 Asp Leu Pro Ser Pro Ser Arg Gln Ala Ser Thr Arg Arg Met Ser Ile  
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gga gag tca att gat gga aaa atc aat gat tgg gaa gag cca agg ctt 240  
 Gly Glu Ser Ile Asp Gly Lys Ile Asn Asp Trp Glu Glu Pro Arg Leu  
 65 70 75

gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa 288  
 Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln  
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aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa 336  
 Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln  
 95 100 105 110

ccg gag cac gaa atg atg cga gtt atg gga acg ata ttc gag aag aag 384  
 Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys  
 115 120 125

cac gcg gaa aat ttt gag acc ttc tgt gag cag ctg ctc gca gtg ccc 432  
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gca tag aca gat caa tgt cca atg tct tat gga cgt ttg ata ggt cta 528  
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ctg cag gga caa gtg cga aac ctc ttc gtt tac aca tcg ctg ttc atc 624  
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 255 260 265

gtg tgt ggg cgg atg atg ttc agc ttg aag taacgtattc aatttgtgta 866  
 Val Cys Gly Arg Met Met Phe Ser Leu Lys



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Tyr Arg Arg Arg Thr Met Ala Thr Gly Glu Met Lys Glu Phe Leu Gly  
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Ile Lys Gly Thr Glu Pro Thr Asp Phe Gly Ile Asn Ser Asp Ala Gln  
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65 70 75  
gat atc gag gga ttt gtg gtc gac tat ttc acg cac cga atc cgg caa 288  
Asp Ile Glu Gly Phe Val Val Asp Tyr Phe Thr His Arg Ile Arg Gln  
80 85 90  
aac gga atg gaa tgg ttt gga gca ccg gga ttg ccg tgt gga gtg caa 336  
Asn Gly Met Glu Trp Phe Gly Ala Pro Gly Leu Pro Cys Gly Val Gln  
95 100 105 110  
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Pro Glu His Glu Met Met Arg Val Met Gly Thr Ile Phe Glu Lys Lys  
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His Ala Glu Asn Phe Glu Thr Phe Cys Glu Gln Leu Leu Ala Val Pro  
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gcc gca tcc cgc gac ccg gtc gcc agg acc tgc ccg ctg cag acc ccg 1683  
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gct gcc ccc ggc gcc gcc gcg ggg cct gcg ctc agc ccg gtg cca cct 1731  
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145

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155

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Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp  
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Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala  
65 70 75 80  
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala  
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Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe  
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Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly  
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Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp  
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